

=> d his

(FILE 'HOME' ENTERED AT 15:05:47 ON 15 AUG 2006)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 15:06:00 ON 15 AUG 2006

```
L1          0 S LT-B-R
L2        637 S LYMPHOTOXIN (3W) BETA (W) RECEPTOR
L3        62 S L2 (S) FUSION
L4        17 S L3 (S) (ADMINISTRATION OR ADMINISTER OR ADMINISTERS OR TREAT
L5          8 DUP REM L4 (9 DUPLICATES REMOVED)
L6          0 S L3 (P) OPHTHALMIA
L7          0 S L2 (P) OPHTHALMIA
L8          0 S L2 (P) OPHTHALMIA
L9       1069 S LYMPHOTOXIN (W) BETA
L10         0 S L9 (P) OPHTHALMIA
L11         0 S SYMPHATHETIC (W) OPHTHALMIA
L12        30 S OPHTHALMIA
L13        30 DUP REM L12 (0 DUPLICATES REMOVED)
L14         0 S L13 (S) (AUTOIMMUNE OR TH)
L15       1131 S SYMPATHETIC (W) OPHTHALMIA
L16         0 S L15 (S) (AUTOIMMUE OR TH)
L17        39 S L15 (S) AUTOIMMUNE
L18        23 DUP REM L17 (16 DUPLICATES REMOVED)
L19         0 S L15 (S) (TH (W) CELL)
```

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1051	Browning.IN.	US-PGPUB; USPAT	OR	ON	2006/08/15 13:52
L2	31	L1 and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:35
L3	28	Benjamin.IN. and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:30
L4	5	Hochman.IN. and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:35

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.ra1.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:31:35 ; Search time 49 Seconds
(without alignments)
351.909 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1133	100.0	197	1	US-08-505-606-1 Sequence 1, Appli
2	1133	100.0	197	2	US-09-000-166-1 Sequence 1, Appli
3	1133	100.0	197	2	US-09-303-262-1 Sequence 1, Appli
4	1133	100.0	473	2	US-09-949-016-7944 Sequence 7944, Ap
5	987	87.1	170	2	US-08-828-683A-14 Sequence 14, Appl
6	981	86.6	170	2	US-09-523-323-57 Sequence 57, Appl
7	771	68.0	415	2	US-09-006-353A-6 Sequence 6, Appli
8	771	68.0	415	2	US-09-573-986-6 Sequence 6, Appli
9	456	40.2	77	2	US-08-866-545-3 Sequence 3, Appli

10	456	40.2	77	2	US-09-627-775-3	Sequence 3, Appli
11	305	26.9	227	2	US-08-974-022-48	Sequence 48, Appl
12	305	26.9	227	2	US-08-795-445A-48	Sequence 48, Appl
13	305	26.9	227	2	US-08-795-447A-48	Sequence 48, Appl
14	305	26.9	227	2	US-08-974-186-48	Sequence 48, Appl
15	305	26.9	227	2	US-08-795-446B-48	Sequence 48, Appl
16	305	26.9	227	2	US-08-706-945D-134	Sequence 134, App
17	305	26.9	227	2	US-08-577-788C-48	Sequence 48, Appl
18	305	26.9	235	2	US-09-326-394-4	Sequence 4, Appli
19	305	26.9	235	2	US-09-580-235-2	Sequence 2, Appli
20	305	26.9	235	2	US-09-580-235-8	Sequence 8, Appli
21	305	26.9	235	2	US-09-580-181-2	Sequence 2, Appli
22	305	26.9	235	2	US-09-580-181-8	Sequence 8, Appli
23	305	26.9	235	2	US-09-102-530-2	Sequence 2, Appli
24	305	26.9	235	2	US-09-102-530-8	Sequence 8, Appli
25	305	26.9	235	2	US-09-882-735A-16	Sequence 16, Appl
26	305	26.9	257	2	US-09-579-845-10	Sequence 10, Appl
27	305	26.9	439	2	US-10-360-101-226	Sequence 226, App
28	305	26.9	461	1	US-08-385-229-2	Sequence 2, Appli
29	305	26.9	461	1	US-08-650-000-2	Sequence 2, Appli
30	305	26.9	461	2	US-09-042-785A-7	Sequence 7, Appli
31	305	26.9	461	2	US-08-477-347-3	Sequence 3, Appli
32	305	26.9	461	2	US-09-006-353A-4	Sequence 4, Appli
33	305	26.9	461	2	US-08-476-862-2	Sequence 2, Appli
34	305	26.9	461	2	US-09-573-986-4	Sequence 4, Appli
35	305	26.9	461	2	US-08-406-824A-2	Sequence 2, Appli
36	305	26.9	461	2	US-09-800-909-2	Sequence 2, Appli
37	305	26.9	461	2	US-09-758-124-2	Sequence 2, Appli
38	305	26.9	461	2	US-09-800-908-3	Sequence 3, Appli
39	305	26.9	461	2	US-09-896-096A-17	Sequence 17, Appl
40	305	26.9	461	2	US-09-949-016-6019	Sequence 6019, Ap
41	305	26.9	461	2	US-10-046-433-6	Sequence 6, Appli
42	305	26.9	461	7	5395760-2	Patent No. 5395760
43	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
44	305	26.9	491	2	US-09-949-016-7840	Sequence 7840, Ap
45	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rapbm.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:43:31 ; Search time 176 Seconds
(without alignments)
518.485 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1133	100.0	197	4	US-10-003-211-1
2	1133	100.0	197	5	US-10-077-406-1
3	1133	100.0	435	3	US-09-907-372-19
4	1133	100.0	435	3	US-09-768-779A-6
5	1133	100.0	435	3	US-09-917-372-19
6	1133	100.0	435	4	US-10-087-192-942
7	1133	100.0	435	4	US-10-291-480-6
8	1133	100.0	435	4	US-10-369-300-17
9	1133	100.0	435	4	US-10-262-445-133
10	1133	100.0	435	6	US-11-077-386-19

11	1133	100.0	450	6	US-11-077-386-20	Sequence 20, Appl
12	1129	99.6	399	3	US-09-907-372-1	Sequence 1, Appli
13	1129	99.6	399	3	US-09-917-372-1	Sequence 1, Appli
14	1129	99.6	399	6	US-11-077-386-18	Sequence 18, Appl
15	1108	97.8	416	5	US-10-484-148-16	Sequence 16, Appl
16	987	87.1	170	4	US-10-112-793-14	Sequence 14, Appl
17	970	85.6	172	4	US-10-375-680-57	Sequence 57, Appl
18	780	68.8	257	3	US-09-948-018-19	Sequence 19, Appl
19	771	68.0	402	4	US-10-087-192-939	Sequence 939, App
20	771	68.0	415	3	US-09-826-212-6	Sequence 6, Appli
21	771	68.0	415	3	US-09-907-372-20	Sequence 20, Appl
22	771	68.0	415	3	US-09-935-727-8	Sequence 8, Appli
23	771	68.0	415	3	US-09-917-372-20	Sequence 20, Appl
24	771	68.0	415	4	US-10-186-643-6	Sequence 6, Appli
25	771	68.0	415	4	US-10-418-242-8	Sequence 8, Appli
26	771	68.0	415	5	US-10-943-197-47	Sequence 47, Appl
27	771	68.0	415	6	US-11-182-946-6	Sequence 6, Appli
28	381.5	33.7	305	4	US-10-264-049-3058	Sequence 3058, Ap
29	311.5	27.5	659	4	US-10-363-427-12	Sequence 12, Appl
30	307	27.1	720	4	US-10-363-427-8	Sequence 8, Appli
31	305	26.9	225	3	US-09-840-795-10	Sequence 10, Appl
32	305	26.9	227	3	US-09-405-032-131	Sequence 131, App
33	305	26.9	227	5	US-10-762-159-131	Sequence 131, App
34	305	26.9	235	3	US-09-102-530-2	Sequence 2, Appli
35	305	26.9	235	3	US-09-102-530-8	Sequence 8, Appli
36	305	26.9	235	3	US-09-907-263-4	Sequence 4, Appli
37	305	26.9	235	3	US-09-882-735-16	Sequence 16, Appl
38	305	26.9	235	4	US-10-243-230-2	Sequence 2, Appli
39	305	26.9	235	4	US-10-243-230-8	Sequence 8, Appli
40	305	26.9	235	4	US-10-436-826-75	Sequence 75, Appl
41	305	26.9	235	4	US-10-621-783-4	Sequence 4, Appli
42	305	26.9	235	4	US-10-622-383-4	Sequence 4, Appli
43	305	26.9	235	6	US-11-126-126-16	Sequence 16, Appl
44	305	26.9	257	4	US-10-313-852-10	Sequence 10, Appl
45	305	26.9	257	4	US-10-314-033-10	Sequence 10, Appl

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:44:06 ; Search time 31 Seconds
(without alignments)
419.700 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1133	100.0	197	6	US-10-533-153-1	Sequence 1, Appli
2	305	26.9	355	6	US-10-504-973-33	Sequence 33, Appl
3	305	26.9	461	6	US-10-511-937-2945	Sequence 2945, Ap
4	305	26.9	461	7	US-11-183-218-32	Sequence 32, Appl
5	295.5	26.1	278	7	US-11-170-797-16	Sequence 16, Appl
6	290	25.6	258	6	US-10-643-589-4	Sequence 4, Appli
7	280	24.7	237	6	US-10-504-973-22	Sequence 22, Appl
8	278	24.5	197	7	US-11-211-917-139	Sequence 139, App

9	278	24.5	277	6	US-10-511-937-2518	Sequence 2518, Ap
10	278	24.5	277	7	US-11-170-797-5	Sequence 5, Appli
11	251.5	22.2	269	7	US-11-170-797-19	Sequence 19, Appl
12	243.5	21.5	289	7	US-11-170-797-12	Sequence 12, Appl
13	239.5	21.1	349	7	US-11-175-714-67	Sequence 67, Appl
14	239.5	21.1	401	7	US-11-175-714-54	Sequence 54, Appl
15	230.5	20.3	283	6	US-10-539-228-546	Sequence 546, App
16	230.5	20.3	283	6	US-10-539-228-548	Sequence 548, App
17	230.5	20.3	283	6	US-10-539-228-550	Sequence 550, App
18	228.5	20.2	655	6	US-10-505-928-843	Sequence 843, App
19	228.5	20.2	655	6	US-10-196-749-418	Sequence 418, App
20	205	18.1	247	6	US-10-504-973-6	Sequence 6, Appli
21	201	17.7	277	6	US-10-511-937-2455	Sequence 2455, Ap
22	198	17.5	153	7	US-11-211-917-140	Sequence 140, App
23	195.5	17.3	255	6	US-10-623-808-8	Sequence 8, Appli
24	195.5	17.3	255	6	US-10-539-257-2	Sequence 2, Appli
25	195.5	17.3	255	7	US-11-128-422-8	Sequence 8, Appli
26	182	16.1	194	6	US-10-539-228-543	Sequence 543, App
27	179.5	15.8	256	6	US-10-623-808-6	Sequence 6, Appli
28	179.5	15.8	256	7	US-11-128-422-6	Sequence 6, Appli
29	172.5	15.2	250	7	US-11-320-192-11	Sequence 11, Appl
30	171.5	15.1	251	7	US-11-320-192-8	Sequence 8, Appli
31	167.5	14.8	440	7	US-11-254-182-49	Sequence 49, Appl
32	156	13.8	411	7	US-11-254-182-47	Sequence 47, Appl
33	156	13.8	411	7	US-11-297-319-1	Sequence 1, Appli
34	152.5	13.5	243	7	US-11-320-192-9	Sequence 9, Appli
35	152.5	13.5	243	7	US-11-320-192-12	Sequence 12, Appl
36	150.5	13.3	250	7	US-11-320-192-10	Sequence 10, Appl
37	148.5	13.1	250	7	US-11-320-192-7	Sequence 7, Appli
38	146.5	12.9	111	7	US-11-211-917-141	Sequence 141, App
39	145	12.8	60	6	US-10-560-025-37	Sequence 37, Appl
40	140.5	12.4	417	6	US-10-505-928-793	Sequence 793, App
41	137.5	12.1	468	6	US-10-511-937-2595	Sequence 2595, Ap
42	133.5	11.8	417	6	US-10-196-749-474	Sequence 474, App
43	132.5	11.7	575	7	US-11-217-997-32	Sequence 32, Appl
44	132.5	11.7	1547	7	US-11-217-997-22	Sequence 22, Appl
45	132.5	11.7	1577	7	US-11-217-997-16	Sequence 16, Appl

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rpr.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:26:35 ; Search time 41 Seconds
(without alignments)
462.310 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1133	100.0	435	2	I54182	tumor necrosis fac
2	305	26.9	461	1	A35356	tumor necrosis fac
3	295	26.0	474	2	B38634	tumor necrosis fac
4	290	25.6	459	2	I48854	gene murine tumour
5	278	24.5	277	2	A60771	B-cell activation
6	243.5	21.5	305	2	A46476	B cell-associated
7	226.5	20.0	651	2	JC7705	death receptor-6 -
8	222.5	19.6	271	2	S12783	OX40 antigen precu
9	214.5	18.9	272	2	I48700	gene ox40 protein
10	210.5	18.6	455	1	GQHUT1	tumor necrosis fac
11	210	18.5	348	2	T28623	hypothetical prote
12	210	18.5	349	2	D36858	gene G4R protein -

13	207	18.3	349	2	D72175	G2R protein - vari
14	206	18.2	461	2	JC4302	tumor necrosis fac
15	201	17.7	277	2	I37552	OX40 homolog - hum
16	201	17.7	454	1	GQMST1	tumor necrosis fac
17	196	17.3	595	2	A42086	CD30 antigen precu
18	195.5	17.3	255	2	I38426	lymphocyte activat
19	189	16.7	325	2	B43692	T2 protein - rabbi
20	187.5	16.5	314	2	I37383	FAS soluble protei
21	184.5	16.3	461	1	GQRTT1	tumor necrosis fac
22	183.5	16.2	326	1	GQVZML	T2 protein - myxom
23	181	16.0	335	2	A40036	apoptosis-mediatin
24	179.5	15.8	256	2	B32393	T-cell antigen 4-1
25	171.5	15.1	425	1	A26431	nerve growth facto
26	166	14.7	493	2	JC5486	membrane glycoprot
27	164	14.5	416	1	JN0006	nerve growth facto
28	162	14.3	327	2	A46484	apoptosis-mediatin
29	148.5	13.1	427	1	GQHUN	nerve growth facto
30	145.5	12.8	324	2	JC2395	Fas antigen precur
31	133	11.7	260	1	A46517	CD27 antigen precu
32	132.5	11.7	1111	2	T26972	hypothetical prote
33	129.5	11.4	1620	2	T27283	hypothetical prote
34	129	11.4	3084	1	MMMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2	T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2	T42017	cysteine rich prot
37	126	11.1	3635	2	T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2	T29764	hypothetical prote
39	124.5	11.0	899	2	G02428	subtilisin-like pr
40	124.5	11.0	915	2	JC6148	subtilisin-like pr
41	124.5	11.0	3707	2	S18252	heparan sulfate pr
42	124	10.9	1680	2	A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2	JC7569	Delta-4 protein -
44	123	10.9	722	2	I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1	A48225	subtilisin-like pr

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rup.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:23:10 ; Search time 300 Seconds
(without alignments)
607.427 Million cell updates/sec

Title: US-10-077-406-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1133	100.0	435	1	TNR3_HUMAN	P36941 homo sapien
2	1098	96.9	435	2	Q5RDW2_PONPY	Q5rdw2 pongo pygma
3	771	68.0	415	1	TNR3_MOUSE	P50284 mus musculu
4	771	68.0	415	2	Q3UK82_MOUSE	Q3uk82 mus musculu
5	749.5	66.2	416	2	Q5U2S8_RAT	Q5u2s8 rattus norv
6	323	28.5	459	2	Q3MHI9_BOVIN	Q3mhi9 bos taurus
7	309.5	27.3	483	2	Q800K7_PAROL	Q800k7 paralichthy
8	305	26.9	461	1	TNR1B_HUMAN	P20333 h tumor nec
9	305	26.9	461	2	Q5THJ6_HUMAN	Q5thj6 homo sapien
10	298.5	26.3	313	2	Q4G265_HORSE	Q4g265 equus cabal
11	295.5	26.1	278	2	Q8SQ34_PIG	Q8sq34 sus scrofa
12	295	26.0	474	1	TNR1B_MOUSE	P25119 mus musculu
13	295	26.0	474	2	Q545P4_MOUSE	Q545p4 m adult mal
14	291.5	25.7	433	2	Q91ZM6_RAT	Q91zm6 rattus norv

15	291.5	25.7	461	2	Q6VAU8_RAT	Q6vau8	rattus norv
16	291.5	25.7	474	1	TNR1B_RAT	Q80wy6	rattus norv
17	291.5	25.7	474	2	Q5YLP0_RAT	Q5ylp0	rattus norv
18	290	25.6	459	2	Q62327_MOUSE	Q62327	mus musculu
19	290	25.6	474	2	Q3U2A9_MOUSE	Q3u2a9	mus musculu
20	285.5	25.2	300	1	TNR6B_HUMAN	O95407	homo sapien
21	284.5	25.1	274	1	TNR5_CANFA	Q7yrl5	canis famil
22	283	25.0	625	1	TNR11_MOUSE	O35305	mus musculu
23	282	24.9	277	2	Q53GN5_HUMAN	Q53gn5	homo sapien
24	280	24.7	274	2	Q3LRP1_CALJA	Q3lrp1	callithrix
25	278	24.5	223	2	Q86YK5_HUMAN	Q86yk5	homo sapien
26	278	24.5	277	1	TNR5_HUMAN	P25942	homo sapien
27	278	24.5	277	2	Q5U007_HUMAN	Q5u007	homo sapien
28	277	24.4	321	2	Q59EP9_HUMAN	Q59ep9	homo sapien
29	277	24.4	616	1	TNR11_HUMAN	Q9y6q6	homo sapien
30	276	24.4	302	2	Q4SNE8_TETNG	Q4sne8	tetraodon n
31	273.5	24.1	280	2	Q3ZTK5_HORSE	Q3ztk5	equus cabal
32	266.5	23.5	387	2	Q6GLN3_XENLA	Q6gln3	xenopus lae
33	265.5	23.4	277	2	Q8WMQ2_SHEEP	Q8wmq2	ovis aries
34	265	23.4	289	2	Q4QQW2_RAT	Q4qqw2	rattus norv
35	258	22.8	275	2	Q3SXX1_MOUSE	Q3sxx1	mus musculu
36	258	22.8	275	2	Q80WM9_MOUSE	Q80wm9	mus musculu
37	258	22.8	276	2	Q71F55_MOUSE	Q71f55	mus musculu
38	253	22.3	462	2	Q5ZL08_CHICK	Q5zl08	gallus gall
39	253	22.3	462	2	Q805B0_CHICK	Q805b0	gallus gall
40	252.5	22.3	203	2	Q5JY15_HUMAN	Q5jy15	homo sapien
41	252.5	22.3	402	2	Q4F9K2_CHICK	Q4f9k2	gallus gall
42	251.5	22.2	269	1	TNR5_BOVIN	Q28203	bos taurus
43	246.5	21.8	401	2	Q6PI12_MOUSE	Q6pi12	mus musculu
44	245	21.6	278	2	Q5BK53_RAT	Q5bk53	rattus norv
45	243.5	21.5	289	1	TNR5_MOUSE	P27512	mus musculu